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0 90
0 10

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RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/891,064A

DATE: 12/26/2001
TIME: 11:39:22

Input Set : A:\754cip.seq.txt
Output Set: N:\CRF3\12262001\I891064A.raw

ENTERED

5 <110> APPLICANT: James M. Anderson
6 Christina M. Van Itallie
8 <120> TITLE OF INVENTION: Human Occludin, Its Uses and Enhancement of Drug
9 Absorption Using Occludin Inhibitors
11 <130> FILE REFERENCE: OCR-754.CIP
13 <140> CURRENT APPLICATION NUMBER: US 09/891,064A
14 <141> CURRENT FILING DATE: 2001-06-25
16 <150> PRIOR APPLICATION NUMBER: US 09/142,732
17 <151> PRIOR FILING DATE: 1998-09-15
19 <160> NUMBER OF SEQ ID NOS: 6
20 <170> SOFTWARE: MS DOS
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24 <211> LENGTH: 2312
26 <212> TYPE: DNA
28 <213> ORGANISM: Homo sapiens
30 <220> FEATURE:
32 <221> NAME/KEY: mat_peptide
34 <222> LOCATION: complete sequence
36 <223> OTHER INFORMATION: human occludin
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41 cgaacgcacc ccgggggtgt cagggacccc catccgtgct gccccctagg 100
42 agcccgccgc tctcctctgc gccccgcctc tcgggcccga acatcgcgcg 150
43 gttccttaa cagcgcgcgt gcagggtgtg ggaagcagga ccgcgtccctc 200
44 ccgcgcgcgc ccatcccgagt ttcaaggtaa ttggtcaccg agggaggagg 250
45 ccgacacacc acacccatcac tccccgcgtcc acctctccct ccctgcttcc 300
46 tcttggcggaa ggcggcagga accgagagcc aggtccagag cgccgaggag 350
47 ccggctctagg acgcagcaga ttggtttata ttggaaagcta aagggcattg 400
48 ctcatcctga agatcagctg accattgaca atcagccatg tcatccaggc 450
49 ctcttggaaatg tccacccct tacaggcctg atgaattcaa accgaatcat 500
50 tatgcaccaa gcaatgacat atatggtgg aagatgcatg ttgcaccaat 550
51 gctctctcag ccagccctact ctttttaccc agaagatgaa attcttact 600
52 tctacaaatg gacctctcct ccaggagtga ttccggatcct gtctatgctc 650
53 attattgtga tgtgcattgc catcttgc tttgtggccct ccacgcttgc 700
54 ctgggacaga ggctatggaa cttccctttt aggaggttagt gttaggctacc 750
55 cttatggagg aagtggctt ggtagctacg gaagtggcta tggctatggc 800
56 tatggttatg gctatggcta cggaggctat acagacccaa gagcagcaaa 850
57 gggcttcatg ttggccatgg ctgcctttt tttcattgcc gcgttggta 900
58 tctttgttac cagtgttata agatctgaaa tgtccagaac aagaagatac 950
59 tacttaagtg tgataatagt gagtgctatc ctgggcatca tgggtttat 1000
60 tgccacaatt gtctatataa tgggagtgaa cccaaactgct cagtcttctg 1050
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62 cctgcagcta ctggactcta cgtggatcag tattttgtatc actactgtgt 1150
63 tggatccc caggaggcca ttggcattgt actggggttc atgattattg 1200
64 tggctttgc tttaataatt ttctttgtcg tgaaaactcg aagaaagatg 1250
65 gacaggtatg acaagtccaa tattttgtgg gacaaggaac acatttatga 1300
66 tgagcagccc cccaaatgtcg aggagtgggt taaaaatgtg tctgcaggca 1350

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67 cacaggacgt gccttcaccc ccatctgact atgtggaaag agttgacagt 1400
 68 cccatggcat actcttccaa tggcaaagtg aatgacaagc gtttttatcc 1450
 69 agagtcttcc tataaatcca cgccggttcc tgaagtgggt caggagcttc 1500
 70 cattaaacttc gcctgtggat gacttcaggc agcctcgta cagcagcgg 1550
 71 ggttaactttg agacacacctc aaaaagagca cctgcaaagg gaagagcagg 1600
 72 aaggtaaaag agaacagagc aagatcacta tgagacagac tacacaactg 1650
 73 gcggcggagtc ctgtgatgag ctggaggagg actggatcag ggaatatacca 1700
 74 cctatcactt cagatcaaca aagacaactg tacaagagga attttgacac 1750
 75 tggcctacag gaatacaaga gcttacaatc agaacttgat gagatcaata 1800
 76 aagaactctc ccgtttggat aaagaatttg atgactatag agaagaaaagt 1850
 77 gaagagtaca tggctgctgc tgatgaatac aatagactga agcaagtgaa 1900
 78 gggatctgca gattacaaaa gtaagaagaa tcattgcaag cagttaaaga 1950
 79 gcaaattgtc acacatcaag aagatggtt gagactatga tagacagaaaa 2000
 80 acatagaagg ctgatgccaa gttgtttgag aaattaagta tctgacatct 2050
 81 ctgcaatctt ctcagaaggc aaatgacttt ggaccataac cccggaaagcc 2100
 82 aaacctctgt gagcatcaca aagttttggg ttgcttaac atcatcagta 2150
 83 ttgaaggcatt ttataaatcg ctttgataa tcaactggc tgaacaactc 2200
 84 caattaagga ttttatgctt taaacattgg ttcttgatt aagaatgaaa 2250
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 99 <221> NAME/KEY: peptide
 101 <222> LOCATION: complete sequence
 103 <223> OTHER INFORMATION: human occludin
 105 <400> SEQUENCE: 2
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 108 5 10 15
 110 Glu Phe Lys Pro Asn His Tyr Ala Pro Ser Asn Asp Ile Tyr Gly
 111 20 25 30
 113 Gly Glu Met His Val Arg Pro Met Leu Ser Gln Pro Ala Tyr Ser
 114 35 40 45
 116 Phe Tyr Pro Glu Asp Glu Ile Leu His Phe Tyr Lys Trp Thr Ser
 117 50 55 60
 119 Pro Pro Gly Val Ile Arg Ile Leu Ser Met Leu Ile Ile Val Met
 120 65 70 75
 122 Cys Ile Ala Ile Phe Ala Cys Val Ala Ser Thr Leu Ala Trp Asp
 123 80 85 90
 125 Arg Gly Tyr Gly Thr Ser Leu Leu Gly Gly Ser Val Gly Tyr Pro
 126 95 100 105
 128 Tyr Gly Gly Ser Gly Phe Gly Ser Tyr Gly Ser Gly Tyr Gly Tyr
 129 110 115 120
 131 Gly Tyr Gly Tyr Gly Tyr Gly Gly Tyr Thr Asp Pro Arg
 132 125 130 135
 134 Ala Ala Lys Gly Phe Met Leu Ala Met Ala Ala Phe Cys Phe Ile
 135 140 145 150

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137 Ala Ala Leu Val Ile Phe Val Thr Ser Val Ile Arg Ser Glu Met
138 155 160 165
140 Ser Arg Thr Arg Arg Tyr Tyr Leu Ser Val Ile Ile Val Ser Ala
141 170 175 180
143 Ile Leu Gly Ile Met Val Phe Ile Ala Thr Ile Val Tyr Ile Met
144 185 190 195
146 Gly Val Asn Pro Thr Ala Gln Ser Ser Gly Ser Leu Tyr Gly Ser
147 200 205 210
149 Gln Ile Tyr Ala Leu Cys Asn Gln Phe Tyr Thr Pro Ala Ala Thr
150 215 220 225
152 Gly Leu Tyr Val Asp Gln Tyr Leu Tyr His Tyr Cys Val Val Asp
153 230 235 240
155 Pro Gln Glu Ala Ile Ala Ile Val Leu Gly Phe Met Ile Ile Val
156 245 250 255
158 Ala Phe Ala Leu Ile Ile Phe Phe Ala Val Lys Thr Arg Arg Lys
159 260 265 270
161 Met Asp Arg Tyr Asp Lys Ser Asn Ile Leu Trp Asp Lys Glu His
162 275 280 285
164 Ile Tyr Asp Glu Gln Pro Pro Asn Val Glu Glu Trp Val Lys Asn
165 290 295 300
167 Val Ser Ala Gly Thr Gln Asp Val Pro Ser Pro Pro Ser Asp Tyr
168 305 310 315
170 Val Glu Arg Val Asp Ser Pro Met Ala Tyr Ser Ser Asn Gly Lys
171 320 325 330
173 Val Asn Asp Lys Arg Phe Tyr Pro Glu Ser Ser Tyr Lys Ser Thr
174 335 340 345
176 Pro Val Pro Glu Val Val Gln Glu Leu Pro Leu Thr Ser Pro Val
177 350 355 360
179 Asp Asp Phe Arg Gln Pro Arg Tyr Ser Ser Gly Gly Asn Phe Glu
180 365 370 375
182 Thr Pro Ser Lys Arg Ala Pro Ala Lys Gly Arg Ala Gly Arg Ser
183 380 385 390
185 Lys Arg Thr Glu Gln Asp His Tyr Glu Thr Asp Tyr Thr Thr Gly
186 395 400 405
188 Gly Glu Ser Cys Asp Glu Leu Glu Glu Asp Trp Ile Arg Glu Tyr
189 410 415 420
191 Pro Pro Ile Thr Ser Asp Gln Gln Arg Gln Leu Tyr Lys Arg Asn
192 425 430 435
194 Phe Asp Thr Gly Leu Gln Glu Tyr Lys Ser Leu Gln Ser Glu Leu
195 440 445 450
197 Asp Glu Ile Asn Lys Glu Leu Ser Arg Leu Asp Lys Glu Leu Asp
198 455 460 465
200 Asp Tyr Arg Glu Glu Ser Glu Glu Tyr Met Ala Ala Ala Asp Glu
201 470 475 480
203 Tyr Asn Arg Leu Lys Gln Val Lys Gly Ser Ala Asp Tyr Lys Ser
204 485 490 495
206 Lys Lys Asn His Cys Lys Gln Leu Lys Ser Lys Leu Ser His Ile
207 500 505 510
209 Lys Lys Met Val Gly Asp Tyr Asp Arg Gln Lys Thr

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210 515 520
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222 <220> FEATURE:
224 <221> NAME/KEY: peptide
226 <223> OTHER INFORMATION: construct used in experiments
228 <400> SEQUENCE: 3
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231 5 10 15
233 Tyr Pro Tyr Gly Gly Ser Gly Phe Gly
234 20
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244 <213> ORGANISM: Artificial Sequence
246 <220> FEATURE:
248 <221> NAME/KEY: peptide
250 <223> OTHER INFORMATION: construct used in experiments
252 <400> SEQUENCE: 4
254 Cys Ser Tyr Gly Ser Gly Tyr Gly Tyr Gly Tyr Gly Tyr
255 5 10 15
257 Gly Tyr Gly Gly Tyr Thr Asp Pro Arg
258 20
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268 <213> ORGANISM: Artificial Sequence
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272 <221> NAME/KEY: peptide
274 <223> OTHER INFORMATION: construct used in experiments
276 <400> SEQUENCE: 5
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281 His Arg Pro Met Leu
282 20
286 <210> SEQ ID NO: 6
288 <211> LENGTH: 11
290 <212> TYPE: PRT
292 <213> ORGANISM: Artificial Sequence
294 <220> FEATURE:
296 <221> NAME/KEY: peptide
298 <223> OTHER INFORMATION: construct used in experiments
300 <400> SEQUENCE: 6
302 Ala Ser Gln Gln Val Tyr Arg Lys Asp Pro Cys
303 5 10

VERIFICATION SUMMARY

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